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Beyond pedigree and towards applied genomics.

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Abstract

In the past two centuries, breeding practices led to more than 400 modern dog breeds showing high genetic drift, small population size without admixing events, increased between-breeds differentiation and inbreeding depression. Inbreeding depression and reduced population sizes are major drawbacks of human-driven selection in the dog species. Therefore, increasing the breed genetic basis is extremely important for their welfare and biodiversity. The availability of efficient and affordable genomic techniques such as dense SNPs arrays, together with the effort of the scientific community, allowed the production of massive genomic data of purebred dogs (Parker et al., 2017; Talenti et al., 2018). However, the 75% of the 1 billion living dogs are free-ranging and breeding (Pilot et al., 2015), with largely unknown ancestry. Genomic tools could be useful in this, in improving welfare and possibly enlarging the genetic basis of small dog populations. In this study, we evaluate a combined approach to assign the ancestors of different admixed and purebred dogs, sampled by saliva swab following European rules and genotyped by the 230K SNP chip. We compared three admixed individuals with 183 breeds and populations, including wild canids and wolves from Talenti et al., 2018. A combination of ranked supervised admixture and haplotype sharing (Beagle 4; Browning & Browning, 2013), allowed us to guess the most likely populations of three different admixed dogs. Results diverged in the three cases. We confirmed the supposed ancestry of one dog, partially confirmed the second dog and defined the third dog as a true mongrel, with 5 different breeds found as top ancestry scores comparable in size and morphology. These results suggest usefulness of genomic metrics in define the make-up even for admixed dogs. The genomic era in this species reached the maturity and this information deserves to be included for a better management of single dog and breeds facing for example health and longevity challenges.

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